## REMARKS

Applicants have amended the specification in order to perfect the priority claim under 35 U.S.C. § 120 and 119(e). This amendment does not constitute new matter, and its entry is respectfully requested.

Applicants have amended the claims in order to expedite prosecution in this case. The amendments to claim 1 are supported throughout the specification in the Figures. See, particularly, pages 16-17, 22-25, 49-54 and original claims 2, 3 and 15. Claim 17 is supported at page 19. As such, these amendments do not constitute new matter, and their entry is respectfully requested.

Turning to the Office Action, Applicants appreciate that no prior art has been cited against the present application.

With respect to the Examiner's statement regarding the priority claim under 35 U.S.C. § 120, Applicants respectfully submit that the amendment to the specification has corrected this.

Turning to the Examiner's comments with respect to the Information Disclosure, as the Examiner notes, an IDS was filed on January 10, 2001. As shown by the attached postcard receipt and the transmittal along with the PTO-1449 (copies are attached hereto), one hundred twenty nine references were submitted. If the Examiner is missing any of these references, Applicants would be pleased to provide copies, but these references have previously been filed.

Claims 1-16 were rejected under 35 U.S.C. § 112, second paragraph.

Applicants respectfully submit that this rejection should be withdrawn for the following reasons.

The present application describes the three-dimensional structure of the HIV-1 gp120 protein, with specific reference to the CD4BS and CB4i epitopes. In view of the description of

the specification, the Figures and the accompanying text, Applicants respectfully submit that there would be no ambiguity as to the terms. As discussed in the background of the application, substantial scientific interest has been directed to the HIV envelope protein since 1985 (see pages 2-3 of the present application). Further, it is explained in the paragraph bridging pages 3 and 4, there are conserved regions, and variable regions, disulfide bonds, loop-like structures, etc.

The present application, as discussed, provides, for example, in Figures 1A, a ribbon drawing of the HIV gp120 glycoprotein representing its three-dimensional structure, and Figures 1B-E are surface diagrams of the three-dimensional structure. Figure 2 shows the molecular surface of the gp120 indicating variability among primate immunodeficiency viruses. Figures 3A-D show the spatial relationship of epitopes on the HIV-1 gp120 glycoprotein. Finally, Figure 4 provides a schematic of the expected arrangement of the HIV-1 gp120 glycoprotein in a trimeric complex.

Accordingly, Applicants respectfully submit that in light of the Figures and the present specification the terms used in the claims would readily be understood. For example, the Examiner questioned how to identify a "cavity." Applicants respectfully submit that by just looking at the Figures one can identify cavities. Applicants explicitly identify the cavity corresponding to the Phe residue at position 43 of the wild type HIV-1 HXBc2 strain. See, particularly, the discussion at page 19, and at 50, lines 17-21. With respect to introducing amino acid at a "defined turn structure," Applicants, again, point out that the skilled artisan knows that when one is talking about a three-dimensional structure the defined turn is the position in the protein chain where the chain turns back on itself. By looking at the Figures, one can readily identify such structures, e.g., the various loops V1/V2, V3, V4 (see, for example, Figure 1A and

Figure 4). In addition, other turns that are readily identified in Figure 4 would be ∠D, ∠E etc. Thus, this term to the skilled artisan is well-known. With respect to disulfide bonds and positions, Applicants explicitly point to the specification at pages 22-25 as indicating how to determine which residues can be used. Moreover, Applicants provide a number of specific amino acid residue positions that can be used.

With respect to the Examiner's concerns regarding the conserved epitopes designated as CD4BS, CD4i or 2G12, Applicants, again, submit that these terms are explicitly defined and explained in the specification. See, particularly, the discussion at pages 49-50 that indicates what CD4i epitopes are and how to identify them. Specific references are given to Figures 1A, 3B, 3C and how those epitopes are determined in Table 2 and the accompanying discussion to them. Again, with respect to the CD4BS epitope, the discussion at pages 50-53 fully explains what this epitope is and how to determine it with respect references to Tables 1, 2 and Figure 3B and C showing gp120 residues involved in the formation of these epitopes as recognized by a number of different representative antibodies. Finally, the 2G12 epitope is described and explained at pages 53-54 with specific reference to Figures 1E, 3A, 3B, 3C and Table 2. Thus, Applicants respectfully submit that these terms as used are terms that the skilled artisan would, in fact, understand, and that the specification explicitly exemplifies this so that there can be no ambiguity for the person of skill in the art.

Accordingly, Applicants respectfully submit that the rejection of claims 1 through 16 pursuant to 35 U.S.C. § 112, second paragraph, should be withdrawn.

Claims 1-16 were rejected pursuant to 35 U.S.C. § 112, first paragraph.

Applicants respectfully submit that this rejection should be withdrawn for the following reasons.

As discussed above with respect to the rejection of the claims pursuant to 35 U.S.C. § 112, second paragraph, these are terms that can clearly be understood. To the extent that some experimentation to identify specific proteins is necessary, Applicants explicitly teach what that experimentation is and how that can be accomplished. For example, with respect to identifying where disulfide residues are introduced into the structure, the application at pages 19-25 teaches how that is done. Moreover, the application exemplifies at page 21 a number of residues that can be used. For example, Pro118-Ala433, Leu122-Gly431, Phe210-Gly380 and Ser256-Phe376. Thus, with respect to the disulfide bonds and the sites where they can be introduced, Applicants teach how it is done and provides four separate pairs that can be used.

With respect to defining turns, the Figures show particular regions and at page 25 provides a specific exemplification – namely, Ile423.

With respect to binding sites, the specification at pages 49-54 explicitly discuss this, provides numerous exemplification and in Table 2 provide explicit exemplification of gp120 amino acids residues implicated as well as in the Examples showing how they are determined. So for example with respect to the Examiner's question regarding to the 2G12 epitope, Table 2 explicitly teaches that it involves the amino acid residues corresponding to the HIV-1 HXBc2 strain positions 295, 297, 334, 386, 392 and 397. Thus, the specific 2G12 epitope is defined with respect to the other two epitopes, the specification, again, provides substantial exemplification of those epitopes and how others meeting the definition can be determined.

Applicants respectfully submit that the skilled artisan given the extensive teaching of the specification and the Examples described therein would have no difficulty with making and using the various embodiments claimed.

Accordingly, Applicants respectfully submit that this rejection of the claims should be withdrawn.

In view of the foregoing, Applicants respectfully submit that all claims are in condition for allowance. Early and favorable action is requested.

If any additional fee is required, please charge Deposit Account No. 50-0850.

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Respectfully submitted,

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